AU 1806

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```
 1                                     SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5          (i) APPLICANT: Le, Junming
 6                         Vilcek, Jan
 7                         Daddona, Peter E.
 8                         Ghrayeb, John
 9                         Knight, David M.
10                         Siegel, Scott A.
11
12         (ii) TITLE OF INVENTION: MONOCLONAL AND CHIMERIC ANTIBODIES
13              SPECIFIC FOR HUMAN TUMOR NECROSIS FACTOR
14
15        (iii) NUMBER OF SEQUENCES: 5
16
17         (iv) CORRESPONDENCE ADDRESS:
18              (A) ADDRESSEE: Browdy and Neimark
19              (B) STREET: 419 Seventh Street, N.W.
20              (C) CITY: Washington
21              (D) STATE: D.C.
22              (E) COUNTRY: USA
23              (F) ZIP: 20004
24
25          (v) COMPUTER READABLE FORM:
26              (A) MEDIUM TYPE: Floppy disk
27              (B) COMPUTER: IBM PC compatible
28              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29              (D) SOFTWARE: PatentIn Release #1.0,
30         Version #1.25
31
32         (vi) CURRENT APPLICATION DATA:
33              (A) APPLICATION NUMBER:  08/013,413
34              (B) FILING DATE: 02-FEB-1993
35              (C) CLASSIFICATION: 436
36
37        (vii) PRIOR APPLICATION DATA:
38              (A) APPLICATION NUMBER: US 07/943,852
39              (B) FILING DATE: 11-SEP-1992
40
41        (vii) PRIOR APPLICATION DATA:
42              (A) APPLICATION NUMBER: US 07/853,606
43              (B) FILING DATE: 18-MAR-1992
44
45        (vii) PRIOR APPLICATION DATA:
46              (A) APPLICATION NUMBER: US 07/670,827
47              (B) FILING DATE: 18-MAR-1991
48
49         (ix) TELECOMMUNICATION INFORMATION:
50              (A) TELEPHONE: 202-628-5197
51              (B) TELEFAX: 202-737-3528
```

```
52
53
54      (2) INFORMATION FOR SEQ ID NO:1:
55
56          (i) SEQUENCE CHARACTERISTICS:
57              (A) LENGTH: 157 amino acids
58              (B) TYPE: amino acid
59              (D) TOPOLOGY: linear
60
61          (ii) MOLECULE TYPE: peptide
62
63          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65          Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
66          1               5                   10                  15
67
68          Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
69                      20                  25                  30
70
71          Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
72                      35                  40                  45
73
74          Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
75              50                  55                  60
76
77          Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
78          65                  70                  75                  80
79
80          Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
81                          85                  90                  95
82
83          Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
84                      100                 105                 110
85
86          Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
87                      115                 120                 125
88
89          Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
90              130                 135                 140
91
92          Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
93          145             ·       150                 155
94
95
96      (2) INFORMATION FOR SEQ ID NO:2:
97
98          (i) SEQUENCE CHARACTERISTICS:
99              (A) LENGTH: 321 base pairs
100             (B) TYPE: nucleic acid
101             (C) STRANDEDNESS: single
102             (D) TOPOLOGY: linear
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103
104        (ii) MOLECULE TYPE: cDNA
105
106
107        (ix) FEATURE:
108              (A) NAME/KEY: CDS
109              (B) LOCATION: 1..321
110
111
112        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
113
114   GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA    48
115   Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
116    1               5                  10                  15
117
118   GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC    96
119   Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
120               20                  25                  30
121
122   ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA   144
123   Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
124           35                  40                  45
125
126   AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC   192
127   Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
128       50                  55                  60
129
130   AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT   240
131   Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
132    65                  70                  75                  80
133
134   GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC   288
135   Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
136               85                  90                  95
137
138   ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA                       321
139   Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
140               100                 105
141
142
143   (2) INFORMATION FOR SEQ ID NO:3:
144
145           (i) SEQUENCE CHARACTERISTICS:
146                 (A) LENGTH: 107 amino acids
147                 (B) TYPE: amino acid
148                 (D) TOPOLOGY: linear
149
150           (ii) MOLECULE TYPE: protein
151
152           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
153
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154    Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
155     1               5               10                  15
156
157    Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
158                 20              25                  30
159
160    Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
161             35                  40                  45
162
163    Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
164         50                  55                  60
165
166    Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
167     65                  70                  75                  80
168
169    Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
170                 85                  90                  95
171
172    Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
173                 100                 105
174
175    (2)  INFORMATION FOR SEQ ID NO:4:
176
177         (i)  SEQUENCE CHARACTERISTICS:
178              (A)  LENGTH: 357 base pairs
179              (B)  TYPE: nucleic acid
180              (C)  STRANDEDNESS: single
181              (D)  TOPOLOGY: linear
182
183        (ii)  MOLECULE TYPE: cDNA
184
185
186        (ix)  FEATURE:
187              (A)  NAME/KEY: CDS
188              (B)  LOCATION: 1..357
189
190
191        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:
192
193    GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA    48
194    Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
195     1               5               10                  15
196
197    TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC    96
198    Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
199                 20              25                  30
200
201    TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT   144
202    Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
203             35                  40                  45
204
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/013,413A*

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205    GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG    192
206    Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
207         50                  55                  60
208
209    TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT    240
210    Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
211     65                  70                  75                  80
212
213    GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT    288
214    Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
215                     85                  90                  95
216
217
218
219    TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA    336
220    Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
221                 100                 105                 110
222
223    GGC ACC ACT CTC ACA GTC TCC                                        357
224    Gly Thr Thr Leu Thr Val Ser
225             115
226
227
228    (2) INFORMATION FOR SEQ ID NO:5:
229
230         (i) SEQUENCE CHARACTERISTICS:
231             (A) LENGTH: 119 amino acids
232             (B) TYPE: amino acid
233             (D) TOPOLOGY: linear
234
235        (ii) MOLECULE TYPE: protein
236
237        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
238
239    Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
240     1                   5                  10                  15
241
242    Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
243                 20                  25                  30
244
245    Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
246                 35                  40                  45
247
248    Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
249         50                  55                  60
250
251    Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
252     65                  70                  75                  80
253
254    Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
255                     85                  90                  95
```

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256
257    Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
258                100                 105                 110
259
260    Gly Thr Thr Leu Thr Val Ser
261            115
262
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/013,413A*

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Line   Error   Original Text

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/08/013,413A*

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< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION   *US/08/013,413A*

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Line   Original Text   Corrected Text